



wwPDB X-ray Structure Validation Summary Report

Mar 12, 2026 – 05:25 AM UTC

PDB ID : 454D / pdb_0000454d
Title : INTERCALATION AND MAJOR GROOVE RECOGNITION IN THE 1.2 Å RESOLUTION CRYSTAL STRUCTURE OF RH[ME2TRIE]PHI BOUND TO 5'-G(5IU)TGCAAC-3'
Authors : Kielkopf, C.L.; Erkkila, K.E.; Hudson, B.P.; Barton, J.K.; Rees, D.C.
Deposited on : 1999-03-03
Resolution : 1.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the  symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references](#) ) were used in the production of this report:

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition

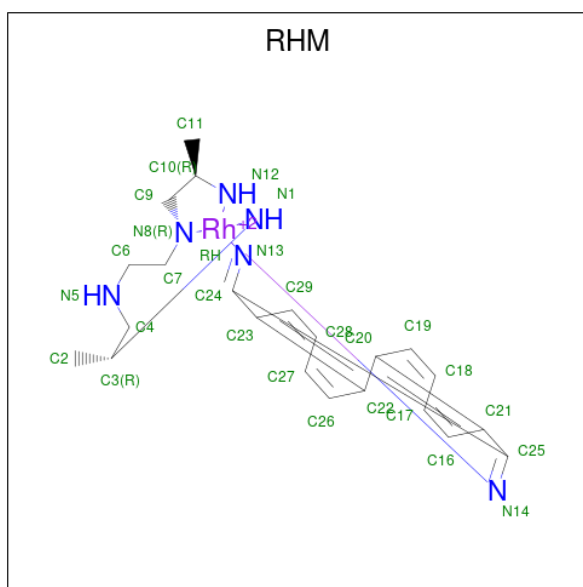
There are 3 unique types of molecules in this entry. The entry contains 2177 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a DNA chain called 5'-D>(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	I	N	O	P			
1	A	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	B	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	C	8	Total 182	C 87	I 1	N 35	O 51	P 8	0	1	0
1	D	8	Total 188	C 88	I 1	N 35	O 55	P 9	0	2	0
1	E	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	F	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	G	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	H	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	I	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0
1	J	8	Total 161	C 77	I 1	N 30	O 46	P 7	0	0	0

- Molecule 2 is DELTA-ALPHA-RH[2R,9R-DIAMINO-4,7-DIAZADECANE]9,10-PHENANTHRENEQUINONE DIIMINE (CCD ID: RHM) (formula: C₂₂H₂₇N₆Rh).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	Rh	0	0
			29	22	6	1		
2	D	1	Total	C	N	Rh	0	0
			29	22	6	1		
2	E	1	Total	C	N	Rh	0	0
			29	22	6	1		
2	G	1	Total	C	N	Rh	0	0
			29	22	6	1		
2	J	1	Total	C	N	Rh	0	0
			29	22	6	1		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	48	Total	O	0	0
			48	48		
3	B	47	Total	O	0	0
			47	47		
3	C	16	Total	O	0	0
			16	16		
3	D	24	Total	O	0	0
			24	24		
3	E	53	Total	O	0	0
			53	53		
3	F	73	Total	O	0	0
			73	73		
3	G	49	Total	O	0	0
			49	49		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	H	31	Total 31	O 31	0	0
3	I	14	Total 14	O 14	0	0
3	J	19	Total 19	O 19	0	0

3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain A: 




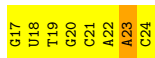
- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain B: 



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain C: 



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain D: 



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain E: 



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'

Chain F: 



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'



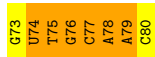
- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'



- Molecule 1: 5'-D(*GP*(5IU)P*TP*GP*CP*AP*AP*C)-3'



4 Data and refinement statistics

Xtrriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	94.74Å 23.98Å 96.52Å 90.00° 93.24° 90.00°	Depositor
Resolution (Å)	17.00 – 1.20	Depositor
% Data completeness (in resolution range)	92.5 (17.00-1.20)	Depositor
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	SHELXL-97	Depositor
R, R_{free}	0.170 , 0.210	Depositor
Estimated twinning fraction	No twinning to report.	Xtrriage
Total number of atoms	2177	wwPDB-VP
Average B, all atoms (Å ²)	32.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: RHM, 5IU

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z >5	RMSZ	# Z >5
1	A	1.07	0/157	1.84	6/238 (2.5%)
1	B	1.10	0/157	1.86	5/238 (2.1%)
1	C	0.97	0/181	2.14	6/275 (2.2%)
1	D	0.95	0/203	1.67	5/309 (1.6%)
1	E	1.08	0/157	1.58	1/238 (0.4%)
1	F	1.00	1/157 (0.6%)	1.51	4/238 (1.7%)
1	G	1.02	1/157 (0.6%)	1.66	5/238 (2.1%)
1	H	0.93	0/157	1.55	2/238 (0.8%)
1	I	0.91	0/157	1.58	4/238 (1.7%)
1	J	0.97	0/157	1.88	6/238 (2.5%)
All	All	1.00	2/1640 (0.1%)	1.74	44/2488 (1.8%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	54	DA	O4'-C1'	5.48	1.52	1.41
1	F	46	DA	O4'-C1'	5.12	1.52	1.41

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	21	DC	P-O3'-C3'	24.32	156.68	120.20
1	A	8	DC	P-O5'-C5'	-10.59	104.11	120.00
1	J	79	DA	P-O5'-C5'	-10.56	104.15	120.00
1	D	29[A]	DC	P-O3'-C3'	9.31	134.16	120.20
1	D	29[B]	DC	P-O3'-C3'	9.31	134.16	120.20

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	161	0	89	1	0
1	B	161	0	89	1	0
1	C	182	0	100	7	0
1	D	188	0	95	6	0
1	E	161	0	89	0	0
1	F	161	0	89	2	0
1	G	161	0	89	1	0
1	H	161	0	89	0	0
1	I	161	0	89	3	0
1	J	161	0	89	13	0
2	B	29	0	25	0	0
2	D	29	0	25	1	0
2	E	29	0	25	0	0
2	G	29	0	25	0	0
2	J	29	0	25	2	0
3	A	48	0	0	2	0
3	B	47	0	0	1	0
3	C	16	0	0	0	0
3	D	24	0	0	1	0
3	E	53	0	0	0	0
3	F	73	0	0	0	0
3	G	49	0	0	1	0
3	H	31	0	0	0	0
3	I	14	0	0	1	0
3	J	19	0	0	2	0
All	All	2177	0	1032	30	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 11.

The worst 5 of 30 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:79:DA:H5''	3:J:326:HOH:O	1.84	0.76
1:D:25:DG:H5'	1:J:80:DC:OP2	1.89	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:J:78:DA:H2'	1:J:78:DA:OP2	1.90	0.71
2:J:85:RHM:H3	2:J:85:RHM:C7	2.21	0.70
1:J:78:DA:H1'	1:J:79:DA:P	2.33	0.69

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

There are no protein molecules in this entry.

5.3.2 Protein sidechains [i](#)

There are no protein molecules in this entry.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

10 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5IU	F	42	1	18,21,22	1.76	3 (16%)	25,30,33	2.09	8 (32%)
1	5IU	E	34	1	18,21,22	1.70	3 (16%)	25,30,33	1.53	5 (20%)
1	5IU	B	10	1	18,21,22	1.67	2 (11%)	25,30,33	1.74	5 (20%)
1	5IU	A	2	1	18,21,22	1.69	2 (11%)	25,30,33	1.67	7 (28%)
1	5IU	J	74	1	18,21,22	1.61	2 (11%)	25,30,33	1.34	4 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	5IU	G	50	1	18,21,22	1.53	2 (11%)	25,30,33	1.82	6 (24%)
1	5IU	I	66	1	18,21,22	1.61	2 (11%)	25,30,33	1.73	7 (28%)
1	5IU	C	18	1	18,21,22	1.56	2 (11%)	25,30,33	1.41	3 (12%)
1	5IU	H	58	1	18,21,22	1.64	2 (11%)	25,30,33	1.97	7 (28%)
1	5IU	D	26	1	18,21,22	1.66	2 (11%)	25,30,33	1.74	7 (28%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	5IU	F	42	1	-	0/7/21/22	0/2/2/2
1	5IU	E	34	1	-	0/7/21/22	0/2/2/2
1	5IU	B	10	1	-	0/7/21/22	0/2/2/2
1	5IU	A	2	1	-	0/7/21/22	0/2/2/2
1	5IU	J	74	1	-	6/7/21/22	0/2/2/2
1	5IU	G	50	1	-	0/7/21/22	0/2/2/2
1	5IU	I	66	1	-	0/7/21/22	0/2/2/2
1	5IU	C	18	1	-	0/7/21/22	0/2/2/2
1	5IU	H	58	1	-	0/7/21/22	0/2/2/2
1	5IU	D	26	1	-	2/7/21/22	0/2/2/2

The worst 5 of 22 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	I	66	5IU	C5-I5	-5.68	1.92	2.08
1	D	26	5IU	C5-I5	-5.50	1.92	2.08
1	C	18	5IU	C5-I5	-5.46	1.92	2.08
1	J	74	5IU	C5-I5	-5.44	1.92	2.08
1	F	42	5IU	O4'-C1'	5.15	1.53	1.42

The worst 5 of 59 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	42	5IU	O4'-C1'-N1	-5.52	98.07	107.86
1	H	58	5IU	C2'-C1'-N1	4.79	125.79	113.81
1	F	42	5IU	C2'-C1'-N1	4.73	125.64	113.81
1	H	58	5IU	O4'-C1'-N1	-4.70	99.53	107.86
1	G	50	5IU	C2'-C1'-N1	4.51	125.08	113.81

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	J	74	5IU	O4'-C4'-C5'-O5'
1	J	74	5IU	C3'-C4'-C5'-O5'
1	J	74	5IU	C2'-C1'-N1-C6
1	J	74	5IU	O4'-C1'-N1-C6
1	J	74	5IU	C2'-C1'-N1-C2

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	J	74	5IU	2	0
1	D	26	5IU	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

5 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	RHM	D	82	-	23,34,34	1.09	0	28,54,54	2.15	8 (28%)
2	RHM	E	83	-	23,34,34	1.06	1 (4%)	28,54,54	1.34	5 (17%)
2	RHM	J	85	-	23,34,34	1.12	1 (4%)	28,54,54	2.49	15 (53%)
2	RHM	G	84	-	23,34,34	1.02	0	28,54,54	1.79	6 (21%)
2	RHM	B	81	-	23,34,34	1.07	1 (4%)	28,54,54	2.12	10 (35%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	RHM	D	82	-	-	-	0/5/6/6
2	RHM	E	83	-	-	-	0/5/6/6
2	RHM	J	85	-	-	-	0/5/6/6
2	RHM	G	84	-	-	-	0/5/6/6
2	RHM	B	81	-	-	-	0/5/6/6

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	83	RHM	C25-N14	2.34	1.37	1.32
2	J	85	RHM	C18-C19	2.16	1.41	1.36
2	B	81	RHM	C28-C29	2.00	1.41	1.36

The worst 5 of 44 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	85	RHM	C9-C10-N12	7.16	120.92	107.36
2	D	82	RHM	C9-C10-N12	7.03	120.67	107.36
2	G	84	RHM	C9-C10-N12	5.53	117.84	107.36
2	B	81	RHM	C9-C10-N12	4.51	115.90	107.36
2	B	81	RHM	C24-C25-C21	-4.17	118.75	121.92

There are no chirality outliers.

There are no torsion outliers.

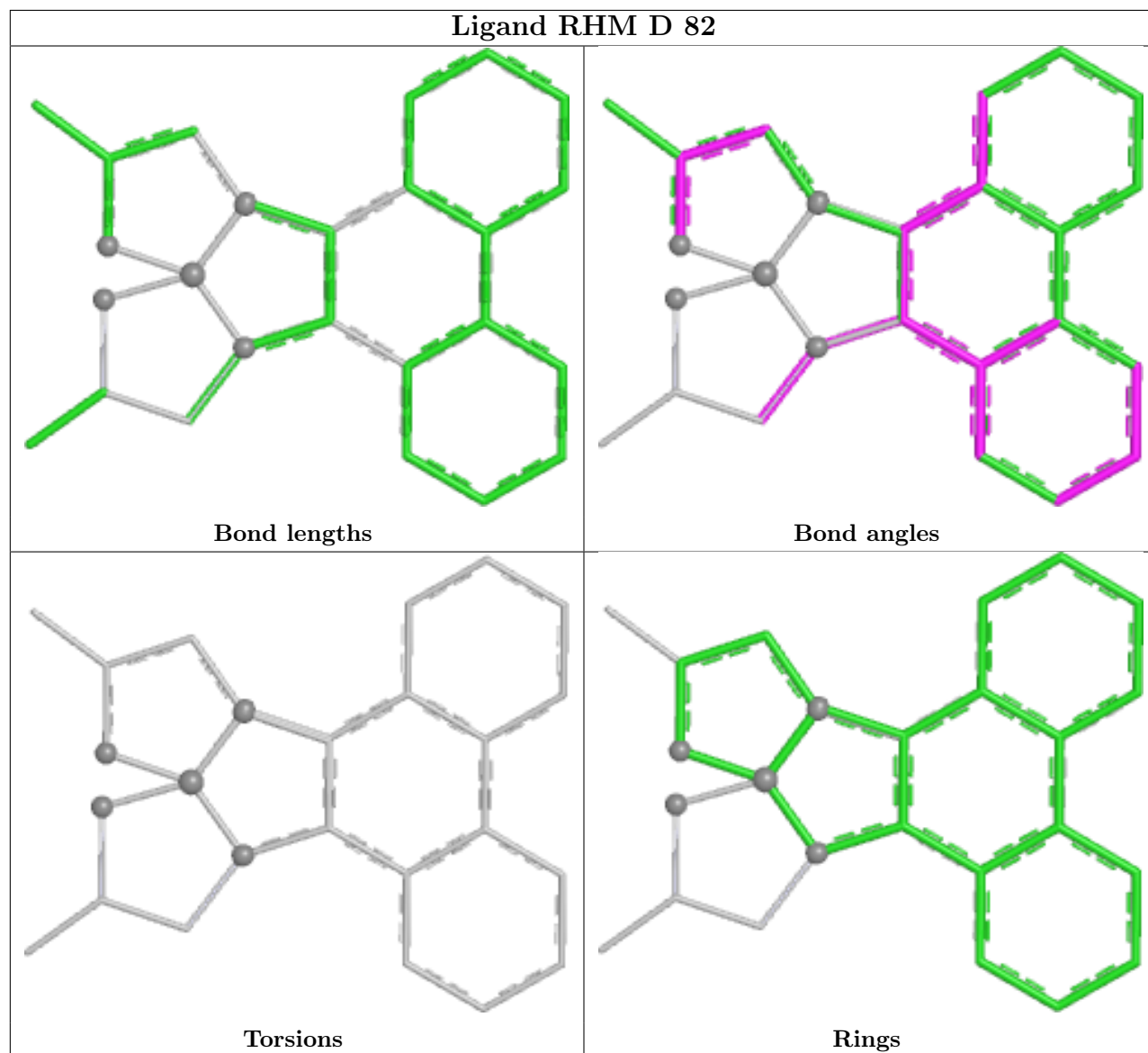
There are no ring outliers.

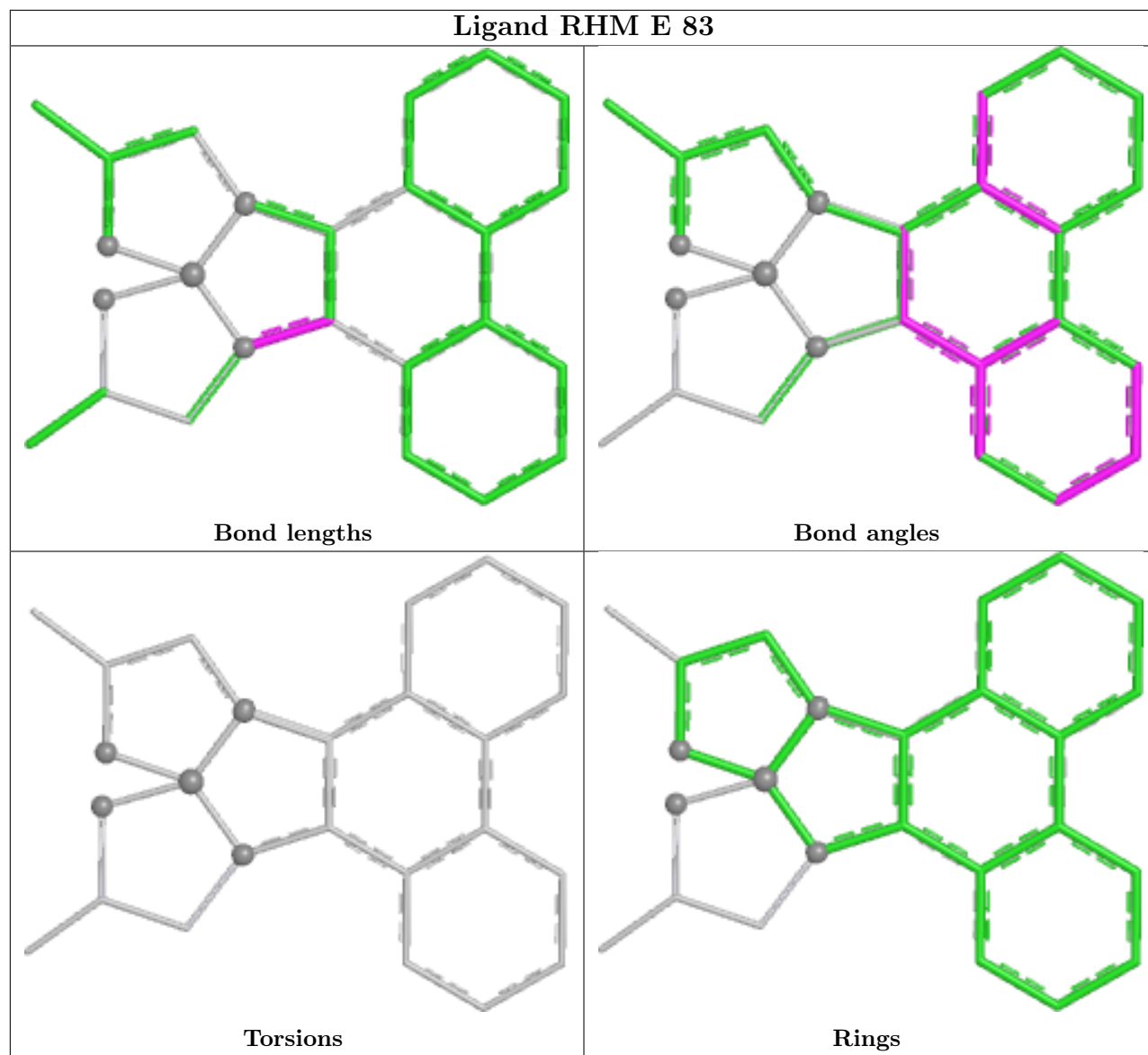
2 monomers are involved in 3 short contacts:

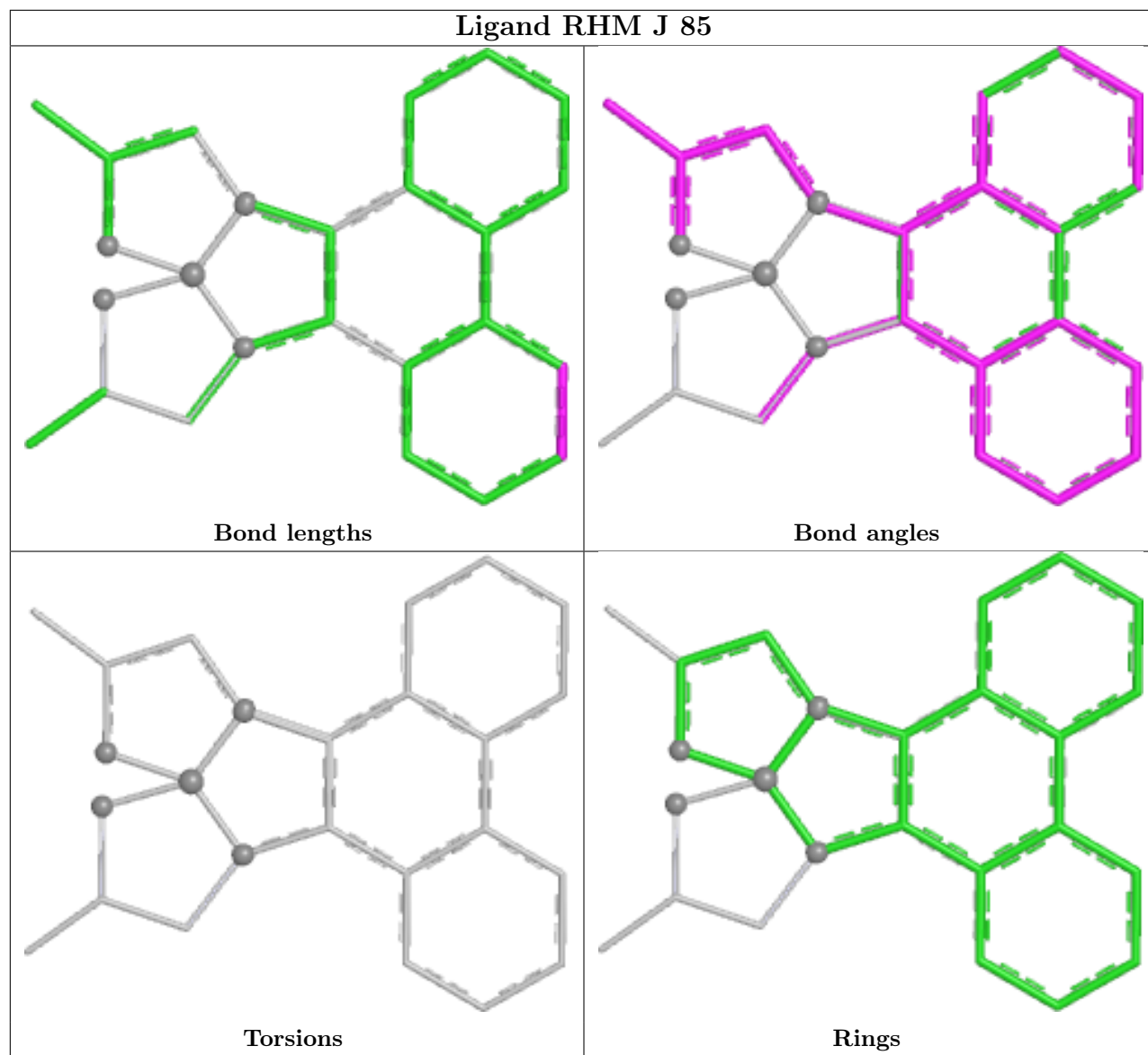
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	82	RHM	1	0
2	J	85	RHM	2	0

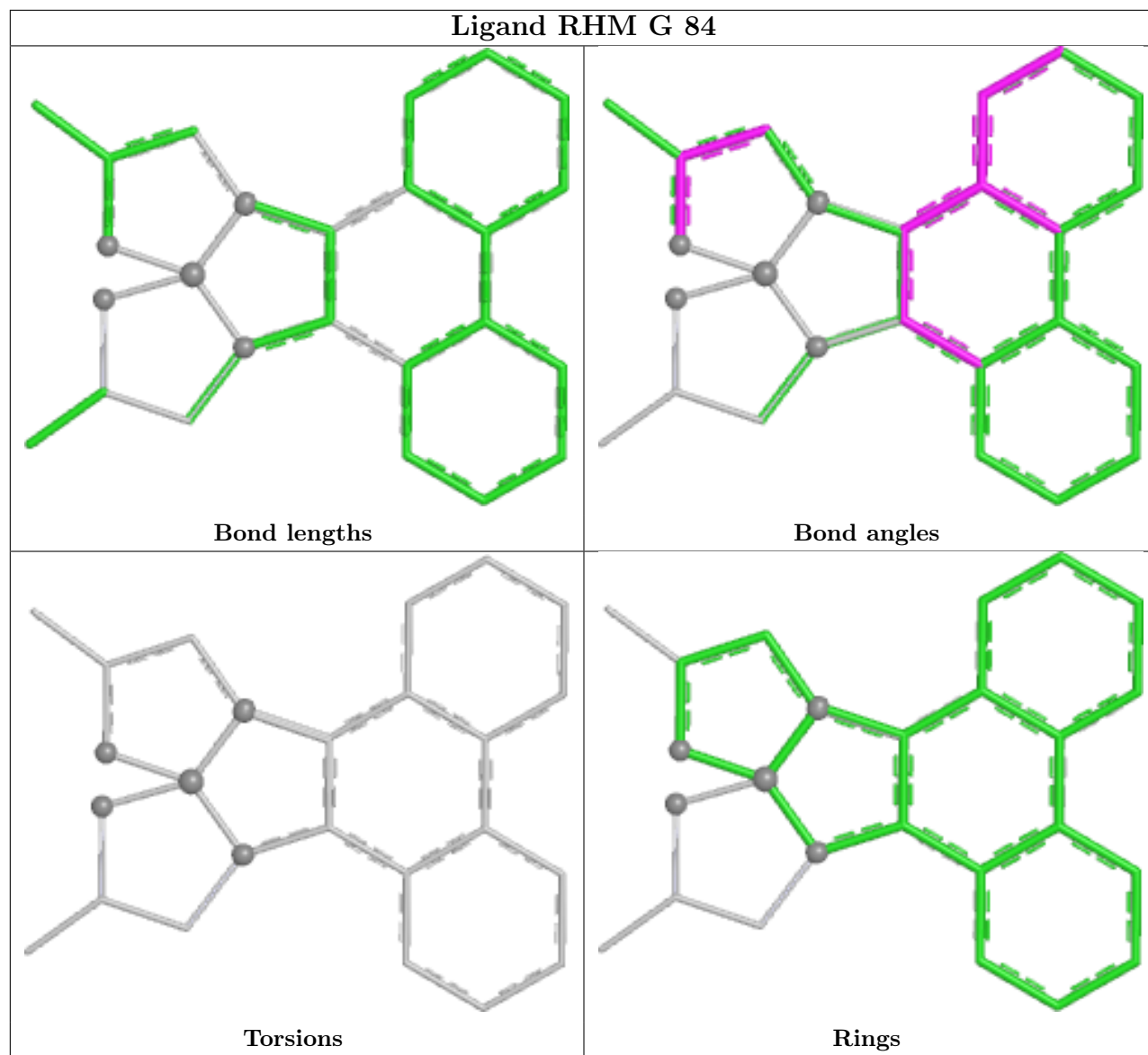
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring

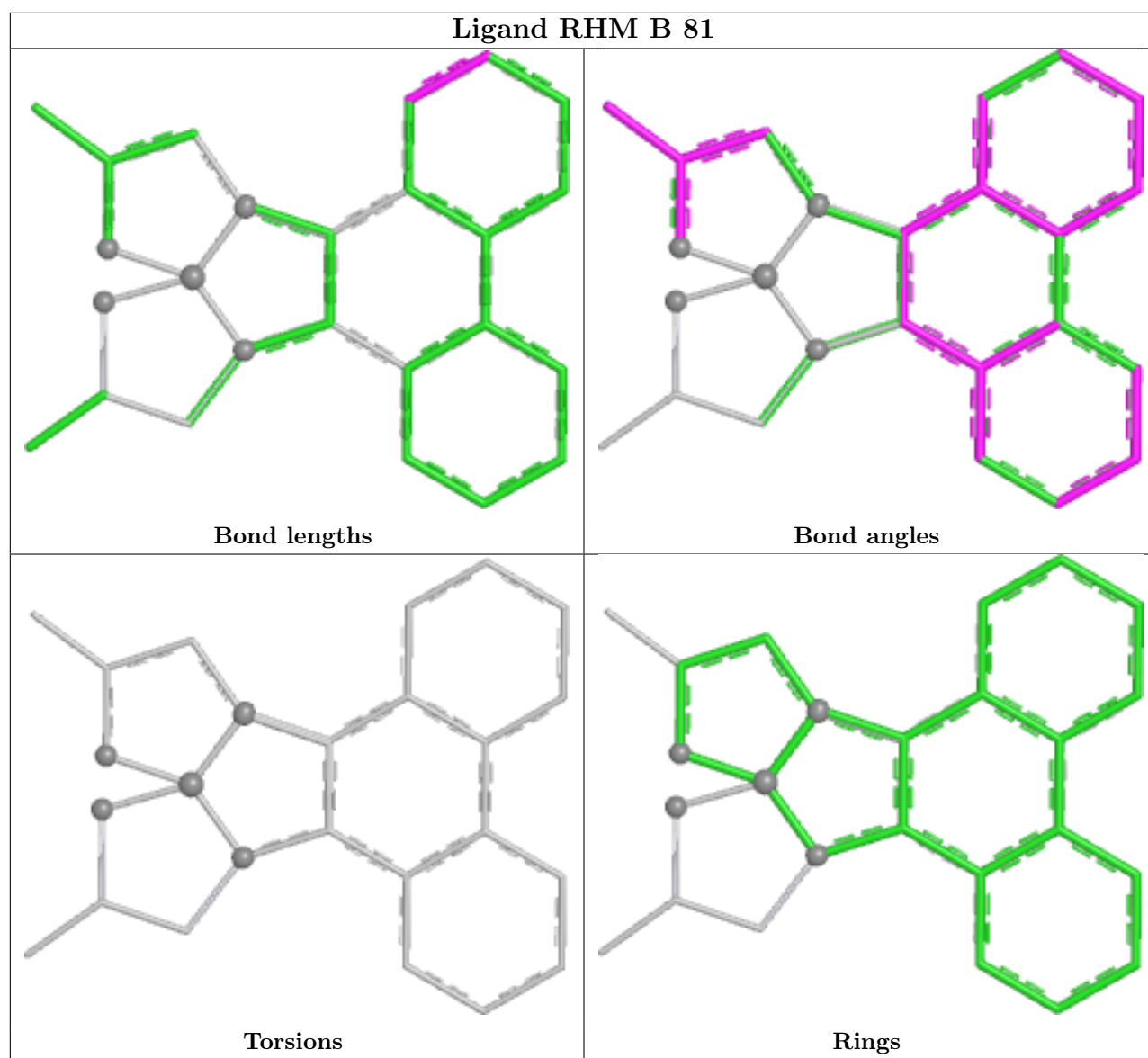
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.











5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.